

FIGURE 1

HSP 90-beta (Mouse)

SEQ ID NO:1

```

1 mpeevhhgee evetfafgae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpskl dsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkhsqfig ypitlyleke rekeisddea eeekgekeee
241 dkdeekpki edvgsdeedd sgdkkkkktk kikekyidqe elnktkpiwt rnpdditgee
301 ygefysltn dwedhlavkh fsvegglefr allfiprrap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremlqgski lkvirknivk kclelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgefv vymtepiday cvqqlkefdg kslsvstkeg
541 lelpedeeek kkmeeskakf enlcklmkei ldkkvekvti snrlvssppc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeadkndka vkdlvllfe
661 tallssgfsl edpqthsnri yrmiklglgi dedevaaeep naavpdeipp legdedasrm
721 eevd

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HSP 90-beta (Human)

SEQ ID NO:2

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1 mpeevhhgee evetfafgae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpskl dsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkhsqfig ypitlyleke rekeisddea eeekgekeee
241 dkdeekpki edvgsdeedd sgdkkkkktk kikekyidqe elnktkpiwt rnpdditgee
301 ygefysltn dwedhlavkh fsvegglefr allfiprrap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremlqgski lkvirknivk kclelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgefv vymtepiday cvqqlkefdg kslsvstkeg
541 lelpedeeek kkmeeskakf enlcklmkei ldkkvekvti snrlvssppc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeadkndka vkdlvllfe
661 tallssgfsl edpqthsnri yrmiklglgi dedevaaeep naavpdeipp legdedasrm
721 eevd

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HSP 90-alpha (Human)

SEQ ID NO:3

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1 mpeetqtqdg pmeeevetf afqaeiaqlm sliintfysn keiflrelis nssdaldkir
61 yesltdpskl dsgkelhinl ipnkqdrtilt ivdtgigmtk adlinnlgti aksgtkafme
121 alqagadism igqfgvgfys aylvaekvtv itkhnddegy awessaggsf tvrtdtgepm
181 grgtkvilhl kedqteylee rriikeivkhh sqfigypitl fvekerdkev sddeaeeked
241 keeekkeek esedkpeied vgsdeeeekk dgdkkkkkki kekyidqeel nktkpiwtrn
301 pdditneeyg efyksltn dw edhlavkhfs vegglefral lfvprapfd lfenrkkknn
361 iklyvrrvfi mdnceelipe ylnfirgvvd sedlplnlsr emlqgskilk virknlvkkc
421 lelftelaed kenyykfyeq fskniklgi edsqrkkls ellryysas gdemvslkdy
481 ctrmkengkh iyyitgetkd qvansafver lrkhgleviy miepidaycv qqlkefegkt
541 lsvstkegle lpedeeekkk geekktkfen lckimkdile kkvekvvsn rlvstspcciv
601 tstygtanm erimkaqalr dnstmgymaa kkhleinp dh sietlrqka eadkndksvk
661 dlvillyeta llssgfsled pqthanriyr miklglgide ddptadddtsa avteempple
721 gdddsrmee vd

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HSP 84 (Mouse)
SEQ ID NO:4

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1 mpeevhhgee evetfafgae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpskldsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkksqfig ypitlyleke rekeisddea eeekgekeee
241 dkedeekpki edvgsdeedd sgdkkkkktk kikekyidqe elnktkpiwt rnpdditqee
301 ygefysltn dwedhlavkh fsvegglefr allfiprrap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremllqgski lkvirknivk kclelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgefv vymtepidey cvqqlkefdg kslsvstkeg
541 lelpedeeek kkmeeskakf enlcklmkei ldkkvekvti snrlvsspcv ivtstygtwa
601 nmerimkaqa lrdnstmgym makkhleinp dhpiivetlrq kaeadkndka vkdlvllife
661 tallssgfsl edpqthsnri yrmiklglgi dedevtaeep saavpdeipp legdedasrm
721 eevd
```

HSP 84 (Human)
SEQ ID NO:5

```
1 mpeevhhgee evetfafgae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpskldsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkksqfig ypitlyleke rekeisddea eeekgekeee
241 dkedeekpki edvgsdeedd sgdkkkkktk kikekyidqe elnktkpiwt rnpdditqee
301 ygefysltn dwedhlavkh fsvegglefr allfiprrap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremllqgski lkvirknivk kclelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgefv vymtepidey cvqqlkefdg kslsvstkeg
541 lelpedeeek kkmeeskakf enlcklmkei ldkkvekvti snrlvsspcv ivtstygtwa
601 nmerimkaqa lrdnstmgym makkhleinp dhpiivetlrq kaeadkndka vkdlvllife
661 tallssgfsl edpqthsnri yrmiklglgi dedevaaeep naavpdeipp legdedasrm
721 eevd
```

HSP 86 (Mouse)
SEQ ID NO:6

```
1 mpeetqtqdg pmeeevetf afgaeiaqlm sliintfysn keiflrelis nssdaldkir
61 yesltdpskl dsgkelhinl ipskqdrtilt ivdtgigmtk adlinnlgti aksgtkafme
121 alqagadism igqfgvgfys aylvaekvtv itkhnddegy awessaggsf tvrtdtgepm
181 grgtkvilhl kedqteylee rrikeivkhh sqfigypitl fvekerdkev sddeaeekke
241 keeekekeek esddkpeied vgsdeeeek kdgdkkkkkk ikekyidqee lnktkpiwtr
301 npdditneey gefyksltn dwedhlavkh fsvegglefra llfvprrapf dlfenrkkkn
361 niklyvrrvf imdnceelip eylnfirgv dsedlplnis remllqgski lkvirknivk
421 clelftelae dkenykkfy qfsknklgi hedsqnrkl sellrytsa sgdemvslkd
481 yctrmkengq hiyfitgetk dqvansafv rlrkhglevi ymiepidey cvqqlkefegk
541 tlsvstkegl elpedeeek kqeeektkfe nlckimkdil ekkvekvvvs nrlvtspcci
601 vtstygtwan merimkaqa lrdnstmgym akkhleinp hsiietlrq aeadkndksv
661 kdlvillyet allssgfsle dpqthanriy rmiklglgid eddptvddts aavteemopl
721 egddtsrme evd
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HSP 86, HSP 60 (Human)
SEQ ID NO:7

```
1 mlrlptvfrq mrpvsrvlap hltrayakdv kfgadaralm lggvdllada vavtmgpkgr
61 tviieqswgs pkvtkdgvtv aksidlkdky knigaklvqd vanntneeag dgtttatvla
121 rsiakegfek iskganpvei rrgvmlavda viaelkkqsk pvttpeeiaq vatisangdk
181 eigniidam kkvgrkgvit vkdgktlnde leiiegmkf d rgyispyfin tskgqkcefq
241 dayvllsekk issiqsiypa leianahrkp lviiaedvdg ealstlvlnr lkvglqvav
301 kapgfgdnrk nqlkdmaiat ggavfgeegl tlnledvqph dlqkvgeviv tkddamllkg
361 kgdkaqiekr iqeiieql dv ttseyekekl nerlaklsdg vavlkvggts ddevnekkdr
421 vtdalnatra aveegivl gg gcallrcipa ldsltpaned qkigieiikr tlkipamtia
481 knagvegsli vekimqssse vgydamagdf vnmvekgiid ptkvvtall daagvasllt
541 taevvvteip keekdpmgga mggmggmgg gm f
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L-plastin (Human)
SEQ ID NO:8

```
1 margsvsdee mmelreafak vtdgngyis fnelndlfka acplpgyrv reitenlmat
61 gdldqdgris fdefikifhg lkstdvaktf rkainkkegi caiggtseqs svgtqhsyse
121 eekyafvwi nkalendpdc rhvipmnpnt ndlfnavgdg ivlckminls vpdtdiderti
181 nkkkltpfti qenlnlaln asaigchvvn igaedlkegk pylvlglwq vikiglfadi
241 elsrnealia llregesled lmklspeell lrwanyhlen agcnkignfs tdikdskayy
301 hllqevapkg deegvpavvi dmsglrekdd igraecmlqg aerlgcrqfv tatdvvrngp
361 klnlafianl fnrypalhkp enqdidwgal egetreertf rnwmnslgvn prvnhllysd
421 sdalvifgly ekikvpvdown rvnkppypkl ggnmklenc nyavelgknq akfslvgigg
481 qdlnegnrtl tlaliwqlmr rytlnileei gggqkvnddi ivnwvnetlr eaeksssis
541 fkdpkistsl pvldlidai pgsinydllk tenlndekl nnakyaisma rkigarvya
601 pedlvevnpk mvmtvfacm gkgmkrv
```

FIG. 2

EL4 Conditioned Media Repels T cells *in vitro*

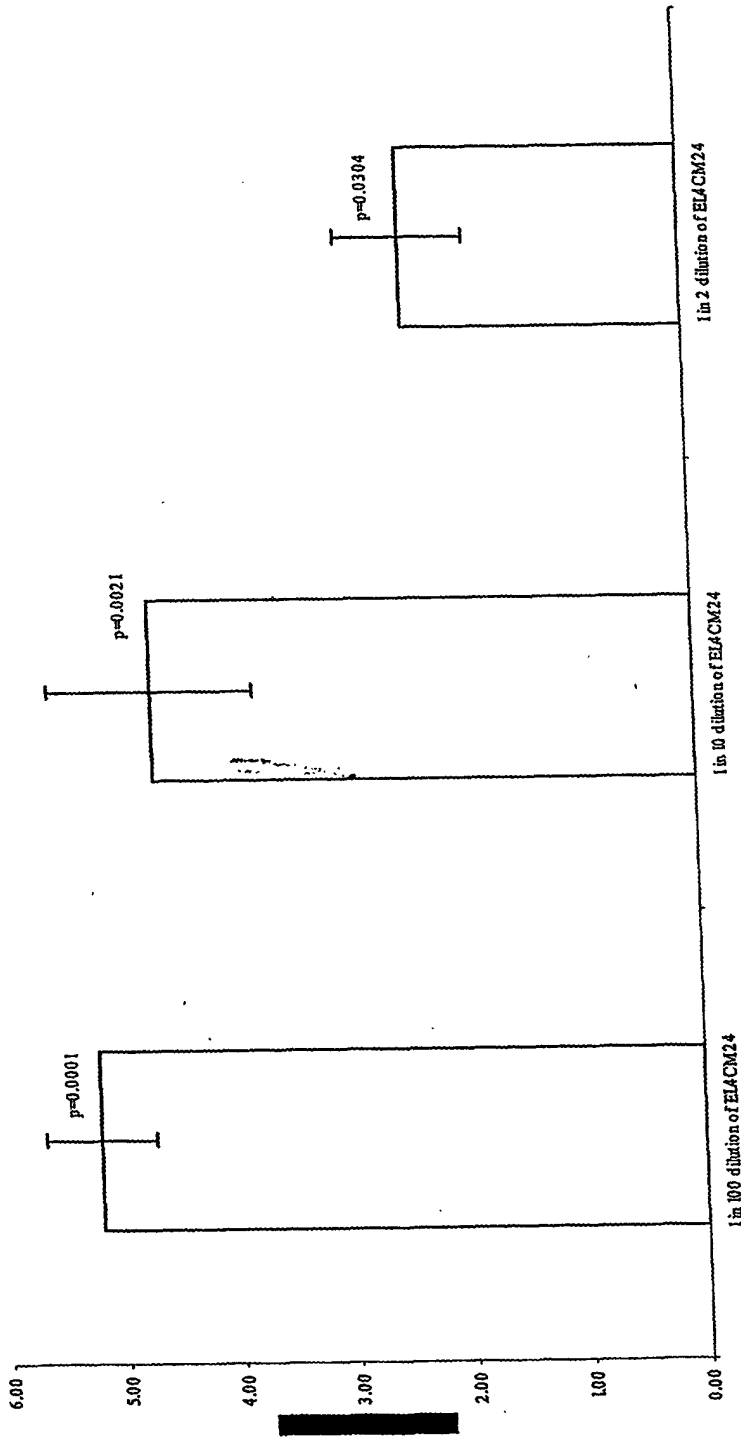
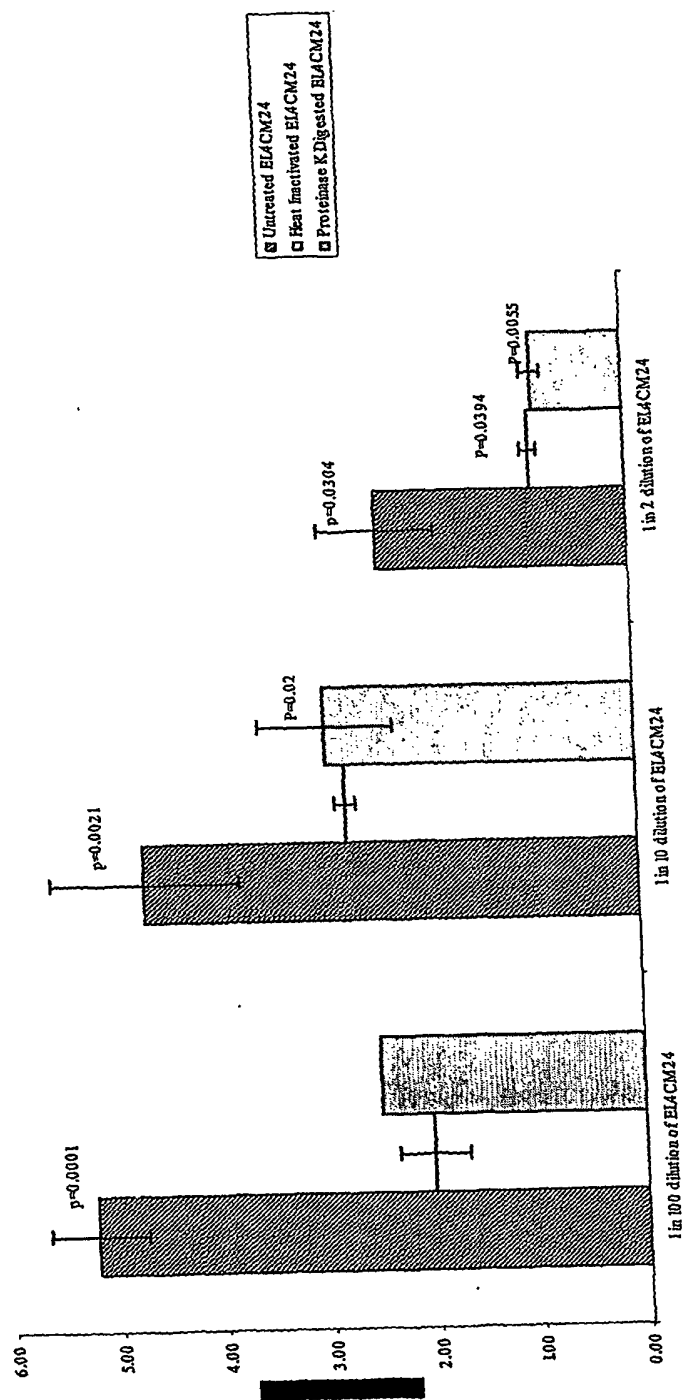


FIG. 3

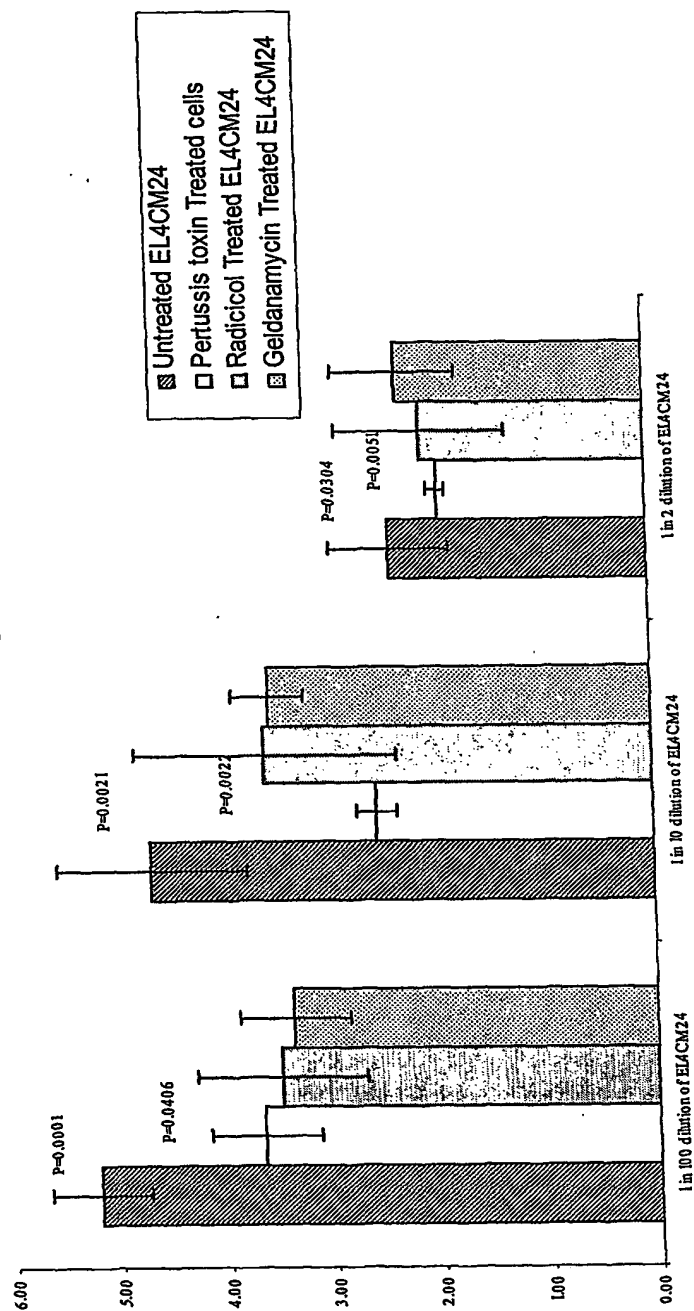
Heat Inactivation and Proteinase K Digestion of EL4CM24



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FIG. 4

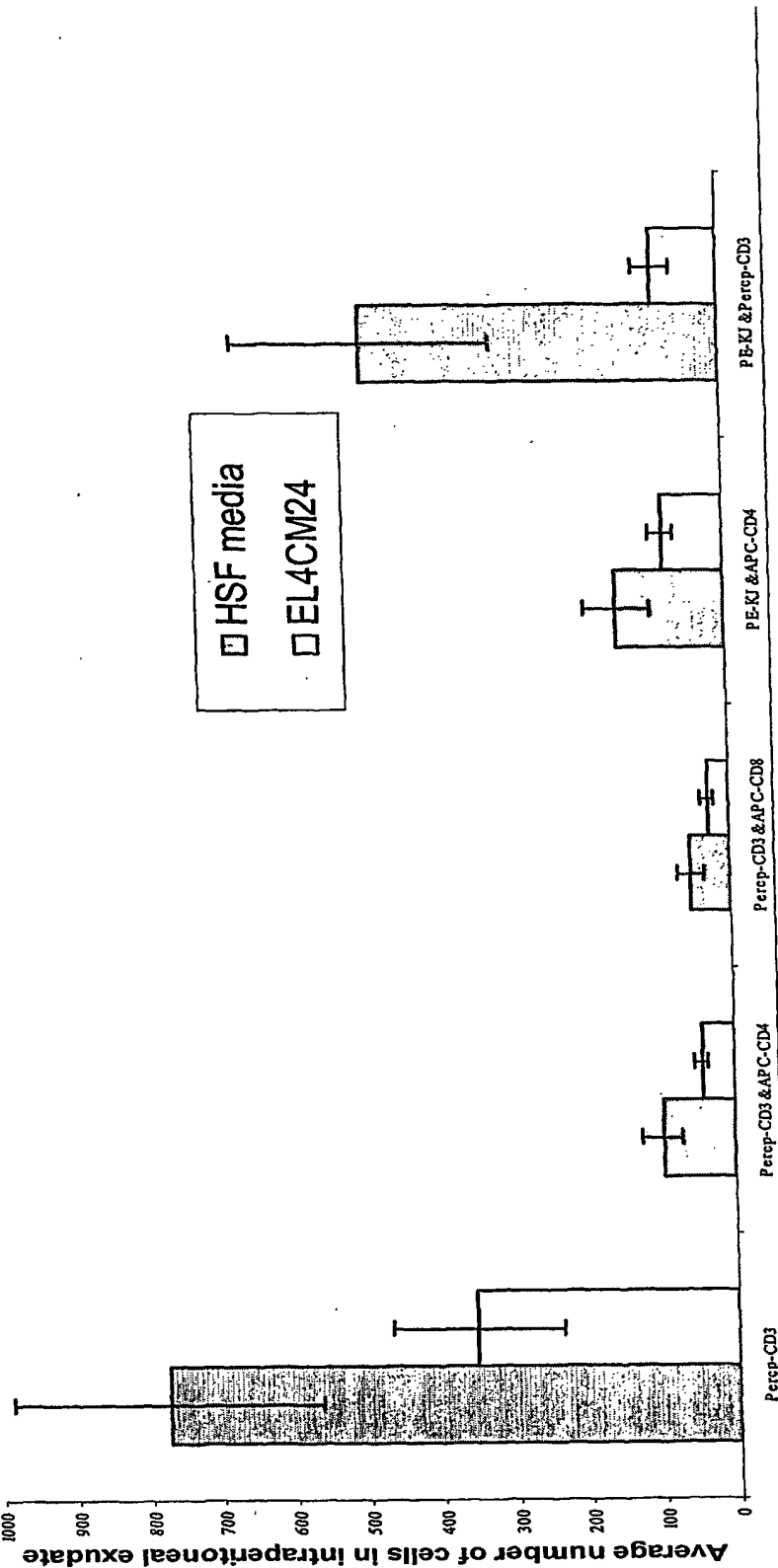
Use of Specific Inhibitors



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FIG. 5

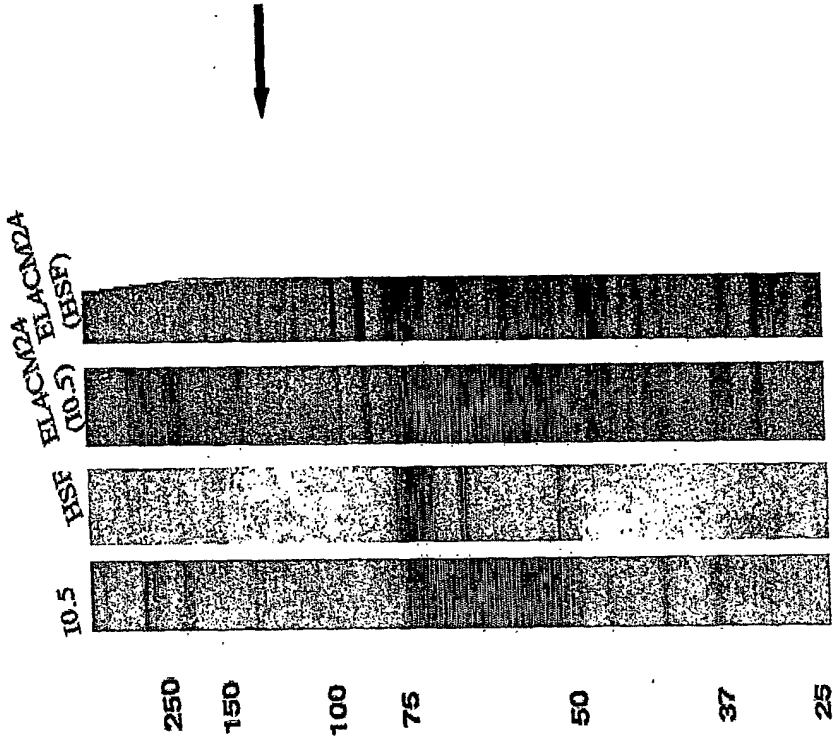
EL4 Conditioned Media Repels T cells *in vivo*



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FIG. 6

EL4CM24 SDS PAGE



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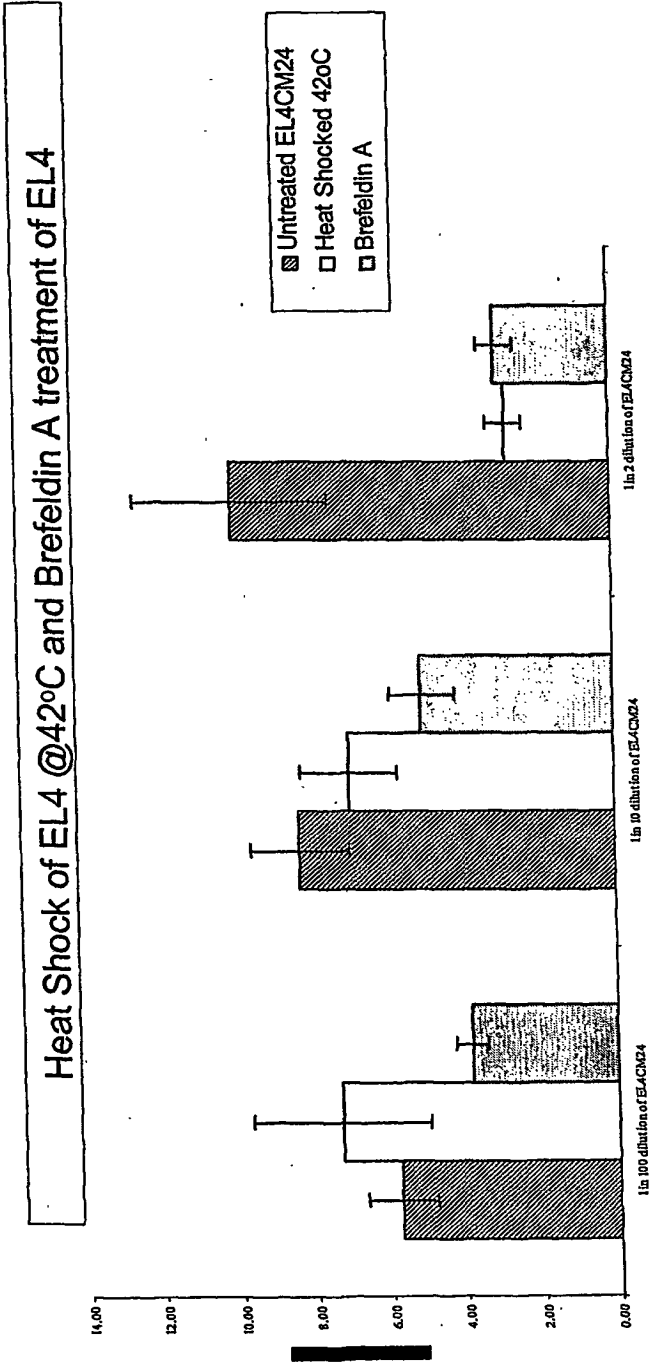
FIG. 7

Ion Exchange Chromatography



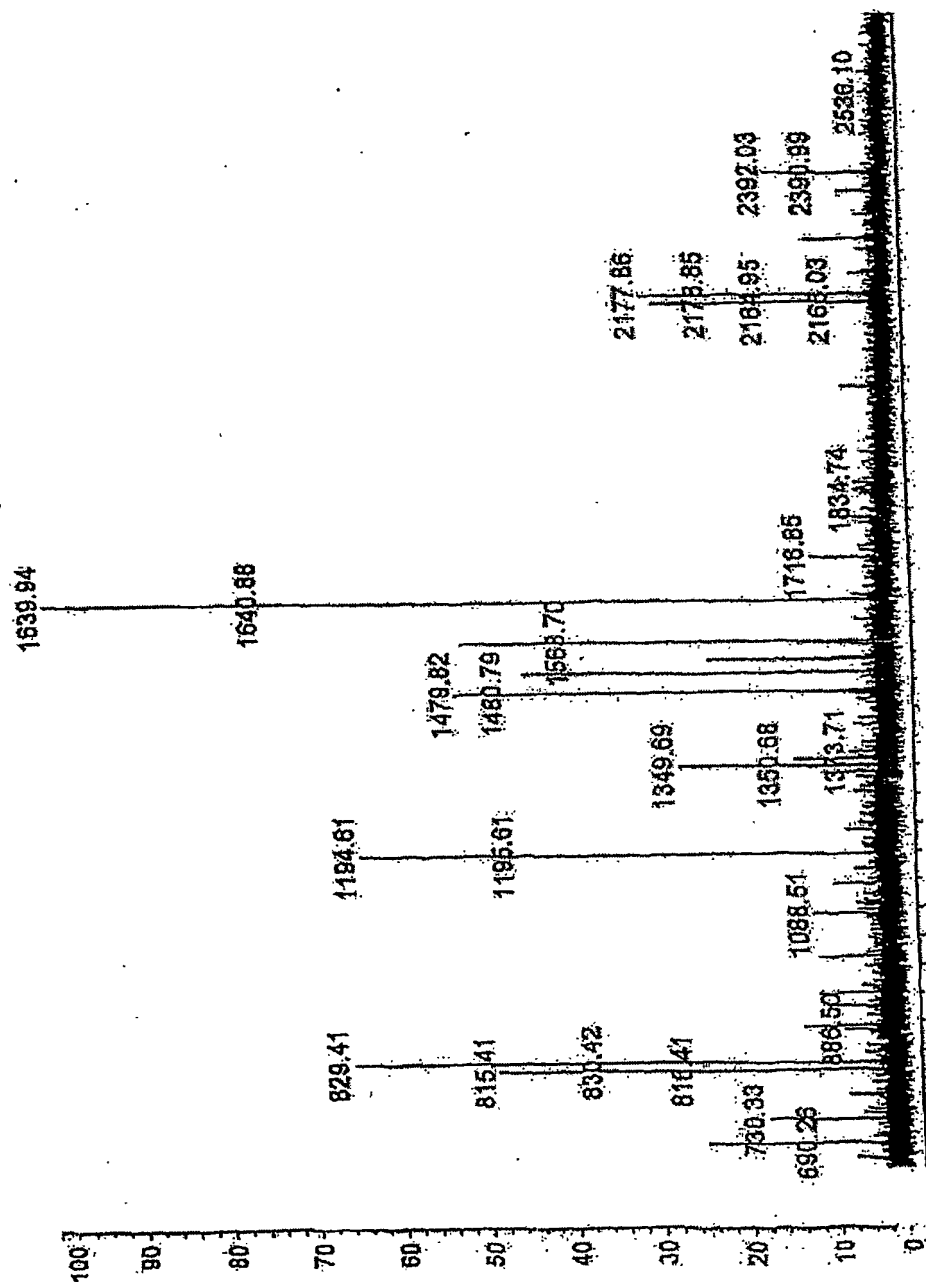
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FIG. 8



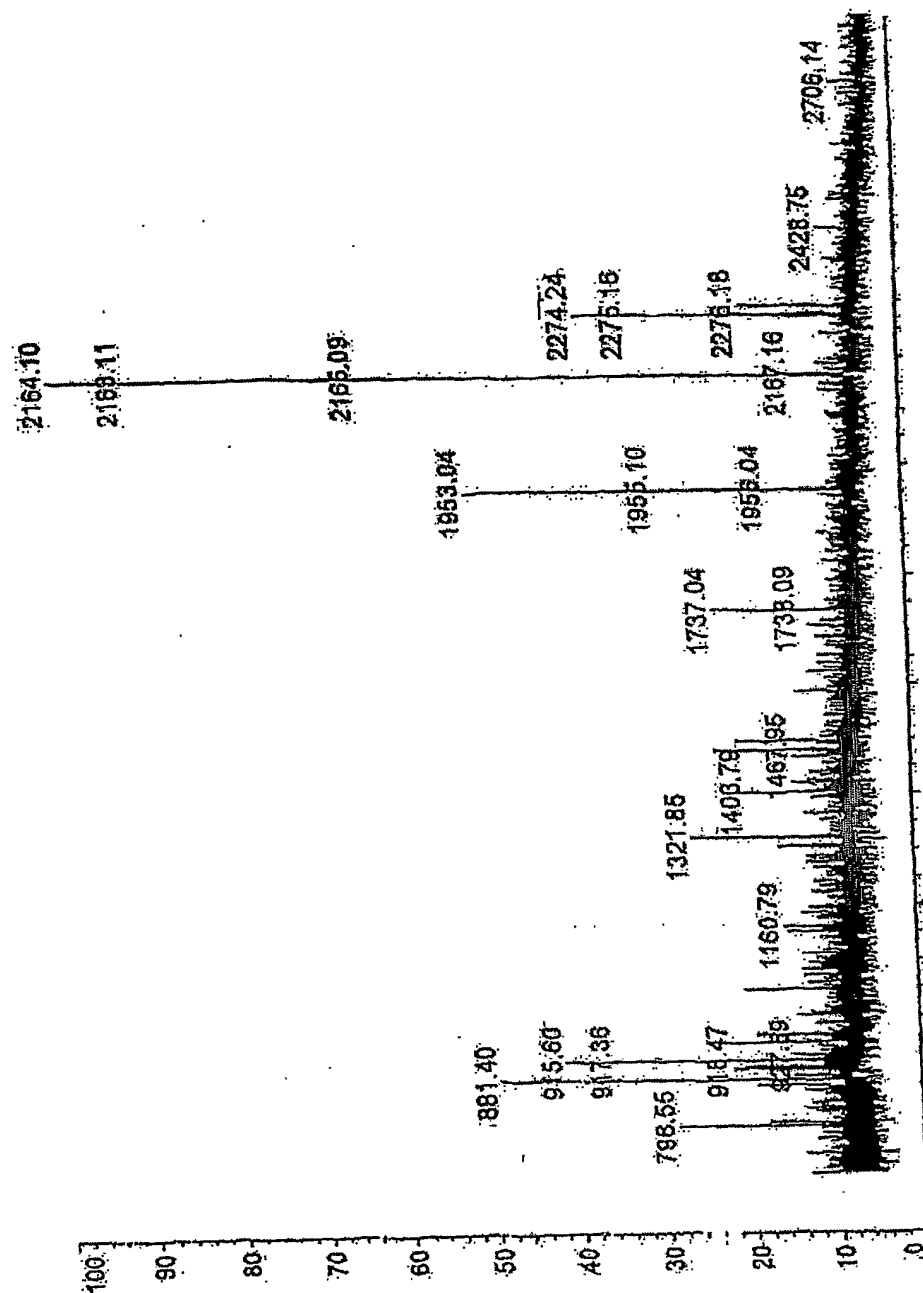
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FIG. 9



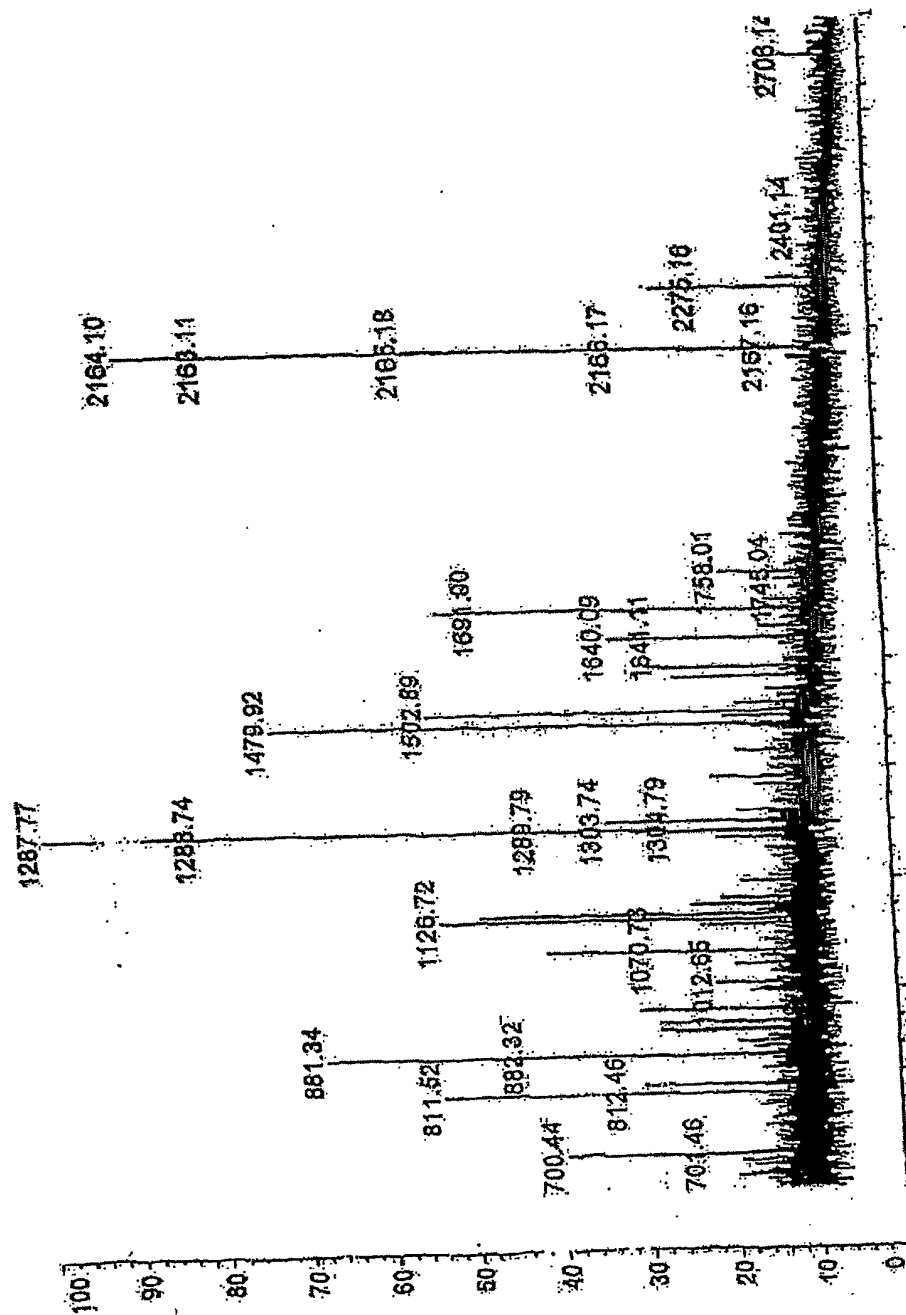
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FIG. 10



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FIG. 11



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FIG. 12A

MS-Fit Search Results

Press stop on your browser if you wish to abort this MS-Fit search prematurely.

Sample ID (comment): Magic Bullet digest
 Database searched: NCBI nr.121002
 Molecular weight search (1000 - 100000 Da) selects 1195692 entries.
 Full pI range: 1247039 entries.
 Species search (MAMMALS) selects 197947 entries.
 Combined molecular weight, pI and species searches select 186900 entries.
 MS-Fit search selects 407 entries (results displayed for top 4 matches):

Considered modifications: [Peptide N-terminal Gln to pyroGln] Oxidation of M [Protein N-terminus Acetylated]

Min. # Peptides to Match	Peptide Mass Tolerance (+/-) ppm	Peptide Masses are monoisotopic	Digest Used Trypsin	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N-terminus Hydrogen (H)	Peptide C-terminus Free Acid (O H)	Input # Peptide Masses
4	150.000			1				15

Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBI nr.121002 Accession #	Protein Name
1	7.02e+003	8/15 (53%)	81963.2 / 4.99	EQUUS CABALLUS	<u>20177936</u>	heat shock protein 90 beta
2	6.91e+003	8/15 (53%)	83264.6 / 4.97	HOMO SAPIENS	<u>20149594</u>	Unknown (protein for MGC:1138)
3	6.79e+003	8/15 (53%)	84843.9 / 5.26	HOMO SAPIENS	<u>11277141</u>	hypothetical protein
4	2.25e+003	7/15 (46%)	83316.8 / 5.06	RATTUS SP.	<u>1346320</u>	heat shock protein 90; hsp90

Detailed Results

1. 8/15 matches (53%), 81963.2 Da, pI = 4.99, Acc. # 20177936, EQUUS CABALLUS, heat shock protein 90 beta.

m/z submitted	MR+ matched	Delta ppm	start and	Peptide Sequence	Modifications
689.3000	689.3946	-137.2410	570	575 (K)VTISNR(L)	
829.4100	829.5300	-144.6415	323	329 (R)ALLFIPR(R)	
891.3500	891.4232	-84.4094	421	427 (K)EYEAESK(N)	
1194.6100	1194.6483	-32.0277	65	74 (K)IDHFNKQER(T)	
1348.6900	1348.6650	18.5557	312	322 (K)RFSVEGQLEFR(A)	
1513.7800	1513.7862	-4.1036	371	384 (R)GVVDSLEPLNISR(R)	
2176.8600	2176.9457	-39.5681	449	467 (R)YHTSQCDEMTSLSEYVSR(M)	
2390.9900	2391.1832	-80.8096	474	494 (K)SIYVITGESKEQVANSATVER(V)	

7 unmatched masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 13% (95/713 AA's) of the protein.
 Coverage Map for This Hit (MS-Digest index #): 1205701

FIG. 12B

2. 8115 matches (33%), 83164.6 Da, pI = 4.97, Acc. # 29149394 HOMO SAPIENS, Unknown protein for MGC:1133).

ms/z	MH ⁺	Delta	start end	Peptide Sequence	Modification
submitted	matched	ppm			
689.3000	689.3946	-137.2410	578 583	(K)YTSNR(L)	
829.4100	829.5300	-144.6415	331 337	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	429 435	(K)PYLAPSK(N)	
1194.6100	1194.6483	-32.0277	73 82	(K)DILPNPQER(T)	
1348.6900	1348.6650	18.5557	320 330	(K)HESVPGDLFFR(A)	
1513.7800	1513.7862	-4.1036	379 391	(R)GVVDSKPLNISR(R)	
2176.8600	2176.9457	-39.3681	457 475	(R)YHTSQSDPMISLSCVSR(Q)	
2390.9900	2391.1832	-80.8096	482 502	(K)SVYTYGSEKQVANSAEVSR(V)	

7 unmatched masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 13% (93/724 AA's) of the protein.
Coverage Map for This Hit (MS-Digest Index #): 137455

3. 8115 matches (33%), 83164.9 Da, pI = 5.26, Acc. # 11277141, HOMO SAPIENS, Hypothetical protein

ms/z	MH ⁺	Delta	start end	Peptide Sequence	Modification
submitted	matched	ppm			
689.3000	689.3946	-137.2410	578 583	(K)YTSNR(L)	
829.4100	829.5300	-144.6415	331 337	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	429 435	(K)PYLAPSK(N)	
1194.6100	1194.6483	-32.0277	73 82	(K)DILPNPQER(T)	
1348.6900	1348.6650	18.5557	320 330	(K)HESVPGDLFFR(A)	
1513.7800	1513.7862	-4.1036	379 391	(R)GVVDSKPLNISR(R)	
2176.8600	2176.9457	-39.3681	457 475	(R)YHTSQSDPMISLSCVSR(Q)	
2390.9900	2391.1832	-80.8096	482 502	(K)SVYTYGSEKQVANSAEVSR(V)	

7 unmatched masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 12% (93/737 AA's) of the protein.
Coverage Map for This Hit (MS-Digest Index #): 130126

4. 7115 matches (46%), 83164.8 Da, pI = 5.06, Acc. # 1346320, RATTUS SP., heat shock protein 90; hsp90.

ms/z	MH ⁺	Delta	start end	Peptide Sequence	Modification
submitted	matched	ppm			
689.3000	689.3946	-137.2410	578 583	(K)YTSNR(L)	
829.4100	829.5300	-144.6415	331 337	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	429 435	(K)PYLAPSK(N)	
1348.6900	1348.6650	18.5557	320 330	(K)HESVPGDLFFR(A)	
1513.7800	1513.7862	-4.1036	379 391	(R)GVVDSKPLNISR(R)	
2176.8600	2176.9457	-39.3681	457 475	(R)YHTSQSDPMISLSCVSR(Q)	
2390.9900	2391.1832	-80.8096	482 502	(K)SVYTYGSEKQVANSAEVSR(V)	

8 unmatched masses: 730.3300 815.4100 1194.6100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

MS-Tag Search Results

Sample ID (numbers): apt A-1 1040AKPVEDLR

Database searched: NCBI nr.121002

Full Molecular Weight range: 1247039 entries

Full pI range: 1247039 entries

Species search: 1040AKPVEDLR 101947 entries

Number of sequences passing through parent score filter: 4253

MS-Tag search select: 7 entries (results displayed for top 3 matches).

Parent mass: 1194.6100 (46.0200 Da)

Fragment ions used in search: 175.31, 212.00, 229.20, 342.61, 355.43, 512.43, 519.50, 616.31, 713.44, 740.51, 866.23 (46.05 Da)

Ion Types Considered: a b y z h i

Search Mode	Max. # Unmatched Ions	Peptide Masses are monoisotopic	Digest Used	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N-Terminus Hydrogen (H)	Peptide C-Terminus Free Acid (A)
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Result Summary

Rank	Unmatched Ions	Sequence	MS/MS Calculated (Da)	MS/MS Error (Da)	Protein MW (Da)	Species	NCBI#121002 Accession #	Protein Name
1	0/11	(K)DILPNPQER(T)	1194.6483	-0.0383	83323.77	4.97 MOUSE	133881	Heat shock protein HSP 90-beta (HSP 90) (Tumor specific transmembrane 84 kDa antigen) (TSTA)
1	0/11	(K)DILPNPQER(T)	1194.6483	-0.0383	83364.17	5.03 MUS MUSCULUS	669305	Heat shock protein, 84 kDa 1
1	0/11	(K)DILPNPQER(T)	1194.6483	-0.0383	14068.47	4.64 HOMO SAPIENS	235110	Heat shock protein beta

FIG. 12C

Detailed Results

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBI nr.121002 Accession #	MS-Digest Index #	Protein Name																																																												
1	0/11	(K)IILPNQPER(T)	1194.6483	-0.0383	83325.7/4.97	MOUSE	123681	318176	Heat shock protein HSP 90-beta (HSP 84) (Tumor specific transfection 84 kDa antigen) (TSTA)																																																												
	0/11	(K)IILPNQPER(T)	1194.6483	-0.0383	83361.1/5.03	MUS MUSCULUS	6680305	583990	heat shock protein, 84 kDa 1																																																												
<table><tr><td>Fragment-Ion (m/z)</td><td>175.31</td><td>212.00</td><td>229.20</td><td>342.62</td><td>355.43</td><td>512.43</td><td>529.50</td><td>626.31</td><td>723.44</td><td>740.58</td><td>966.73</td></tr><tr><td>Ion-type</td><td>y₁</td><td>NP</td><td>b₁</td><td>b₃</td><td>PQE</td><td>y₂-NH₃</td><td>y₄</td><td>y₅-NH₃</td><td>y₆-NH₃</td><td>y₆</td><td>y₈</td></tr><tr><td>Delta Da</td><td>0.19</td><td>-0.10</td><td>0.08</td><td>0.42</td><td>0.27</td><td>0.18</td><td>0.23</td><td>0.02</td><td>0.10</td><td>0.21</td><td>0.19</td></tr><tr><td></td><td></td><td></td><td>D1</td><td>D11</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr><tr><td></td><td></td><td></td><td>0.04</td><td>0.42</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr></table>										Fragment-Ion (m/z)	175.31	212.00	229.20	342.62	355.43	512.43	529.50	626.31	723.44	740.58	966.73	Ion-type	y ₁	NP	b ₁	b ₃	PQE	y ₂ -NH ₃	y ₄	y ₅ -NH ₃	y ₆ -NH ₃	y ₆	y ₈	Delta Da	0.19	-0.10	0.08	0.42	0.27	0.18	0.23	0.02	0.10	0.21	0.19				D1	D11											0.04	0.42							
Fragment-Ion (m/z)	175.31	212.00	229.20	342.62	355.43	512.43	529.50	626.31	723.44	740.58	966.73																																																										
Ion-type	y ₁	NP	b ₁	b ₃	PQE	y ₂ -NH ₃	y ₄	y ₅ -NH ₃	y ₆ -NH ₃	y ₆	y ₈																																																										
Delta Da	0.19	-0.10	0.08	0.42	0.27	0.18	0.23	0.02	0.10	0.21	0.19																																																										
			D1	D11																																																																	
			0.04	0.42																																																																	
1	0/11	(K)IILPNQPER(T)	1194.6483	-0.0383	14066.7/4.64	HOMO SAPIENS	1251110	587097	heat shock protein beta																																																												
<table><tr><td>Fragment-Ion (m/z)</td><td>175.31</td><td>212.00</td><td>229.20</td><td>342.62</td><td>355.43</td><td>512.43</td><td>529.50</td><td>626.31</td><td>723.44</td><td>740.58</td><td>966.73</td></tr><tr><td>Ion-type</td><td>y₁</td><td>NP</td><td>b₁</td><td>b₃</td><td>PQE</td><td>y₂-NH₃</td><td>y₄</td><td>y₅-NH₃</td><td>y₆-NH₃</td><td>y₆</td><td>y₈</td></tr><tr><td>Delta Da</td><td>0.19</td><td>-0.10</td><td>0.08</td><td>0.42</td><td>0.27</td><td>0.18</td><td>0.23</td><td>0.02</td><td>0.10</td><td>0.21</td><td>0.19</td></tr><tr><td></td><td></td><td></td><td>D1</td><td>D11</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr><tr><td></td><td></td><td></td><td>0.08</td><td>0.42</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr></table>										Fragment-Ion (m/z)	175.31	212.00	229.20	342.62	355.43	512.43	529.50	626.31	723.44	740.58	966.73	Ion-type	y ₁	NP	b ₁	b ₃	PQE	y ₂ -NH ₃	y ₄	y ₅ -NH ₃	y ₆ -NH ₃	y ₆	y ₈	Delta Da	0.19	-0.10	0.08	0.42	0.27	0.18	0.23	0.02	0.10	0.21	0.19				D1	D11											0.08	0.42							
Fragment-Ion (m/z)	175.31	212.00	229.20	342.62	355.43	512.43	529.50	626.31	723.44	740.58	966.73																																																										
Ion-type	y ₁	NP	b ₁	b ₃	PQE	y ₂ -NH ₃	y ₄	y ₅ -NH ₃	y ₆ -NH ₃	y ₆	y ₈																																																										
Delta Da	0.19	-0.10	0.08	0.42	0.27	0.18	0.23	0.02	0.10	0.21	0.19																																																										
			D1	D11																																																																	
			0.08	0.42																																																																	

MS-Tag Search Results

Sample ID (comment): Apo A-1 1040 AKPVLEDLR
 Database searched: NCBI nr.121002
 Molecular weight search (1000 - 100000 Da) selects 1195697 entries.
 Full pI range: 1147039 entries.
 Species search (MAMMALS) selects 197947 entries.
 Combined molecular weight, pI and species searches select 186900 entries.
 Number of sequences passing through parent mass filter: 4989
 MS-Tag search selects 18 entries (results displayed for top 3 matches).
 Parent mass: 815.5100 (+/- 0.0000 Da)
 Fragment Ions used in search: 185.26, 255.27, 272.34, 298.32, 354.45, 371.53, 417.39, 445.25, 518.35 (+/- 0.50 Da)
 Ion Types Considered: a b y n h i

Search Mode	Max. # Unmatched Ions	Peptide Masses are monoisotopic	Digest Used	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O H)
Identity	1		Trypsin	1			

Result Summary

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBI nr.121002 Accession #	Protein Name
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	75541.0/5.28	MUS MUSCULUS	20882565	similar to heat shock protein 86
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	84674.2/4.94	HOMO SAPIENS	123678	90 kDa heat-shock protein (AA 1-732)
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	57068.0/6.38	HOMO SAPIENS	12804541	hypothetical protein LOC63929

Detailed Results

Rank	# Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW (Da)/pI	Species	NCBI nr.121002 Accession #	MS-Digest Index #	Protein Name																														
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	75541.0/5.28	MUS MUSCULUS	20882565	815811	similar to heat shock protein 86																														
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	84674.2/4.94	HOMO SAPIENS	123678	162860	90 kDa heat-shock protein (AA 1-732)																														
<table border="1"> <tr> <td>Fragment-Ion (m/z)</td><td>185.26</td><td>255.27</td><td>272.34</td><td>298.32</td><td>354.45</td><td>371.53</td><td>417.39</td><td>445.25</td><td>518.35</td></tr> <tr> <td>Ion-type</td><td>b₁</td><td>y₂-NH₃</td><td>y₂</td><td>b₃</td><td>y₅-NH₃</td><td>y₃</td><td>b₄</td><td>b₄</td><td>y₈</td></tr> <tr> <td>Delta Da</td><td>0.13</td><td>0.12</td><td>0.17</td><td>0.11</td><td>0.24</td><td>0.29</td><td>0.10</td><td>-0.03</td><td>0.04</td></tr> </table>										Fragment-Ion (m/z)	185.26	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35	Ion-type	b ₁	y ₂ -NH ₃	y ₂	b ₃	y ₅ -NH ₃	y ₃	b ₄	b ₄	y ₈	Delta Da	0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04
Fragment-Ion (m/z)	185.26	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35																														
Ion-type	b ₁	y ₂ -NH ₃	y ₂	b ₃	y ₅ -NH ₃	y ₃	b ₄	b ₄	y ₈																														
Delta Da	0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04																														
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	57068.0/6.38	HOMO SAPIENS	12804541	171353	hypothetical protein LOC63929																														
<table border="1"> <tr> <td>Fragment-Ion (m/z)</td><td>185.26</td><td>255.27</td><td>272.34</td><td>298.32</td><td>354.45</td><td>371.53</td><td>417.39</td><td>445.25</td><td>518.35</td></tr> <tr> <td>Ion-type</td><td>b₁</td><td>y₂-NH₃</td><td>y₂</td><td>b₃</td><td>y₅-NH₃</td><td>y₃</td><td>b₄</td><td>b₄</td><td>y₈</td></tr> <tr> <td>Delta Da</td><td>0.13</td><td>0.12</td><td>0.17</td><td>0.11</td><td>0.24</td><td>0.29</td><td>0.10</td><td>-0.03</td><td>0.04</td></tr> </table>										Fragment-Ion (m/z)	185.26	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35	Ion-type	b ₁	y ₂ -NH ₃	y ₂	b ₃	y ₅ -NH ₃	y ₃	b ₄	b ₄	y ₈	Delta Da	0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04
Fragment-Ion (m/z)	185.26	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35																														
Ion-type	b ₁	y ₂ -NH ₃	y ₂	b ₃	y ₅ -NH ₃	y ₃	b ₄	b ₄	y ₈																														
Delta Da	0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04																														

FIG. 13A

MS-Fit Search Results

Sample ID (comment): Magic Bullet digest
 Database searched: NCBI nr.S1403
 Molecular weight search (1000 - 100000 Da) selects 1421445 entries.
 Full pI range: (432416 entries).
 Species search (HUMAN RODENT) selects 214838 entries.
 Combined molecular weight, pI and species searches select 222557 entries.
 MS-Fit search selects 5 entries (results displayed for top 3 matches).

Considered modifications: 1 Peptide N-terminal Cln to pyroGlu | Oxidation of M | Protein N-terminus Acetylated |

Min. # Peptides to Match	Peptide Mass Tolerance (+/-) ppm	Peptide Masses are monoisotopic	Digest Used Trypsin	Max. # Missed Cleavages 1	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (OH)	Input # Peptide Masses 13
7	150.000							

Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBI nr.S1403 Accession #	Protein Name
1	1.81e+003	7/13 (53%)	94057.0 / 5.13	RATTUS NORVEGICUS	24025637	ischemia responsive 94 kDa protein
2	449	7/13 (53%)	94081.1 / 5.13	MUS MUSCULUS	13277753	heat shock protein 4
3	449	7/13 (53%)	94133.1 / 5.15	MUS MUSCULUS	6680301	apc-2

Detailed Results

1. 7/13 matches (53%), 94057.0 Da, pI = 5.13, Acc. # 24025637, RATTUS NORVEGICUS, ischemia responsive 94 kDa protein.

m/z submitted	MW matched	Delta ppm	start	end	Peptide Sequence	Modifications
798.5500	798.4514	123.4893	431	436	(K)VLTRYR(K)	
949.6100	949.5219	92.7425	62	69	(K)NYVGFKR(F)	
1323.8500	1323.7116	104.7200	222	234	(K)VLATAFDITLGR(K)	
1402.7800	1402.6313	106.0213	619	629	(K)NAVEEYVYEMR(D)	
1495.8400	1495.7029	91.6785	20	33	(R)AGGNETIANEYSDR(C)	
1736.0700	1735.9271	82.3407	391	405	(R)EESITDVVPYISLR(W)	
1953.0400	1952.8336	105.6759	406	421	(R)WNSPAERGSSDCEVFPK(N)	

1 unmatched masses: 915.6000 917.3600 1305.8400 1478.8800 1587.9500 1624.0500

The matched peptides cover 10% (84/840 AA's) of the protein.
 Coverage Map for This Hit (MS-Digest Index #): 787619

2. 7/13 matches (53%), 94081.1 Da, pI = 5.13, Acc. # 13277753, MUS MUSCULUS, heat shock protein 4

FIG. 13B

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence	Modifications
798.5500	798.4514	123.4893	431	436	(K) <u>YLTRYR</u> (K)	
949.6100	949.5219	92.7425	62	69	(K) <u>NTVOGPKR</u> (F)	
1305.8400	1305.7418	75.1849	670	680	(K) <u>QVYVDKLAELK</u> (S)	
1321.8500	1321.7116	104.7200	222	234	(K) <u>VLATAFDITLGGR</u> (K)	
1402.7800	1402.6313	106.0213	620	630	(K) <u>NAVEEYVYEMR</u> (D)	
1495.8400	1495.7029	91.6785	20	33	(R) <u>AGGIETIANEYSDK</u> (C)	
1736.0700	1735.9271	82.3407	391	405	(R) <u>EFSITDVVFPYISLR</u> (W)	

6 unmatched masses: 915.6000 917.3600 1478.8800 1587.9500 1624.0500 1953.0400

The matched peptides cover 9% (78/841 AA's) of the protein.
Coverage Map for This Hit (MS-Digest index #): 302745

2. 7/13 matches (53%), 94133.1 Da, pI = 5.15, Acc. # 6680301, MIIIS MUSCULUS, app. 2.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence	Modifications
798.5500	798.4514	123.4893	431	436	(K) <u>YLTRYR</u> (K)	
949.6100	949.5219	92.7425	62	69	(K) <u>NTVOGPKR</u> (F)	
1305.8400	1305.7418	75.1849	670	680	(K) <u>QVYVDKLAELK</u> (S)	
1321.8500	1321.7116	104.7200	222	234	(K) <u>VLATAFDITLGGR</u> (K)	
1402.7800	1402.6313	106.0213	620	630	(K) <u>NAVEEYVYEMR</u> (D)	
1495.8400	1495.7029	91.6785	20	33	(R) <u>AGGIETIANEYSDK</u> (C)	
1736.0700	1735.9271	82.3407	391	405	(R) <u>EFSITDVVFPYISLR</u> (W)	

6 unmatched masses: 915.6000 917.3600 1478.8800 1587.9500 1624.0500 1953.0400

The matched peptides cover 9% (78/841 AA's) of the protein.
Coverage Map for This Hit (MS-Digest index #): 1129227

FIG. 14A

MS-Fit Search Results

Sample ID (construct): Magic Bullet digest
 Database searched: NCBI nr.51403
 Molecular weight search (1000 - 100000 Da) selects 1372760 entries.
 Full pf range: 1432416 entries.
 Species search: (HUMAN RODENT) selects 224838 entries
 Combined molecular weight, pf and species searches select 21465 entries.
 MS-Fit search selects 335 entries (results displayed for top 3 matches).

Considered modifications: [Peptide N-terminal C₁₆ to pyroGlu] Oxidation of M [Protein N-terminus Acetylated]

Mjn. # Peptides to Match	Peptide Mass Tolerance (+/-) ppm	Peptide Masses are monoisotopic	Digest Used Trypsin	Max. # Missed Cleavages 1	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O: H)	Input # Peptide Masses 17
4	150,000	monoisotopic	Trypsin	1	acrylamide	Hydrogen (H)	Free Acid (O: H)	17

Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBI nr.51403 Accession #	Protein Name
1	1.22e+005	11/17 (64%)	70149.7 / 5.20	MUS MUSCULUS	<u>29840803</u>	unnamed protein product
2	1.22e+005	11/17 (64%)	70163.8 / 5.24	MUS MUSCULUS	<u>26326929</u>	unnamed protein product
3	2.66e+004	10/17 (58%)	70201.8 / 5.28	MUS MUSCULUS	<u>6679385</u>	65-kDa macrophage protein

Detailed Results

11/17 matches (64%). 70149.7 Da, pI = 5.20, Acc #29840803, MUS MUSCULUS, unnamed protein product.

m/z submitted, matched	MH ⁺ Delta ppm	start end	Peptide Sequence	Modifications
700.4400	700.4146	36.2352	77 82 (K)VFHGLK(S)	
811.5200	811.4136	131.0872	585 591 (K)YALSMAR(K)	
942.5800	942.5413	47.0831	442 449 (R)VNKPEVPK(L)	
1069.7200	1069.6257	88.1285	264 272 (K)LSPEELLIR(W)	
1126.7200	1126.6373	73.4015	433 441 (K)IKVPVDWNR(V)	
1135.7100	1135.6111	87.0474	348 357 (R)QEVATDVR(G)	
1287.7700	1287.6268	111.2008	402 412 (R)NVMNSLCVNPR(V)	
1502.8900	1502.7525	91.5194	166 178 (K)MINLSVPTIDER(T)	
1585.9400	1585.8477	58.1710	597 610 (R)YYALPEDLVEYNPK(M)	
1689.9700	1689.8560	67.4478	473 488 (K)ESLVGIACODINEGNR(T)	
1758.0100	1757.8744	77.1528	310 326 (K)GPRGIFAVVIDMSCLR(E)	

unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900

the matched peptides cover 19% (120/627 AA's) of the protein.

FIG. 14B

Coverage Map for This Hit (MS-Digest index #): 372720

2. 11/17 matches (64%). 70163.8 Da, pI = 5.24; Acc. # 26326929. MUS MUSCULUS, unnamed protein product.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence	Modifications
700.4400	700.4146	36.2352	77	82	(K)VFHGLK(S)	
811.5200	811.4136	131.0872	585	591	(K)YALSMAR(K)	
942.5800	942.5413	41.0831	442	449	(R)YVKFPYPK(L)	
1069.7200	1069.6257	88.1285	264	272	(K)LSPEELILR(W)	
1126.7200	1126.6373	73.4015	433	441	(K)IKVPVDWNR(V)	
1135.7100	1135.6111	87.0474	348	357	(R)QFYATDVVR(G)	
1287.7700	1287.6268	111.2008	402	412	(R)NWMNSLGVNPR(V)	
1502.8900	1502.7525	91.5194	166	178	(K)MINLSVPDTIDER(T)	
1585.9400	1585.8477	58.1710	597	610	(R)YYALPEDLVEVNPK(M)	
1689.9700	1689.8560	67.4478	473	488	(K)ESLVGIACODLNENR(T)	
1758.0100	1757.8744	77.1528	310	326	(K)GDEEGIPAVVIDMSGLR(E)	

6 unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900

The matched peptides cover 19% (120/627 AA's) of the protein.
Coverage Map for This Hit (MS-Digest index #): 1174311

3. 10/17 matches (58%). 70201.8 Da, pI = 5.28; Acc. # 6679385. MUS MUSCULUS, 65-kDa macrophage protein.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence	Modifications
700.4400	700.4146	36.2352	77	82	(K)VFHGLK(T)	
811.5200	811.4136	131.0872	585	591	(K)YALSMAR(K)	
942.5800	942.5413	41.0831	442	449	(R)YVKFPYPK(L)	
1069.7200	1069.6257	88.1285	264	272	(K)LSPEELILR(W)	
1126.7200	1126.6373	73.4015	433	441	(K)IKVPVDWNR(V)	
1135.7100	1135.6111	87.0474	348	357	(R)QFYATDVVR(G)	
1287.7700	1287.6268	111.2008	402	412	(R)NWMNSLGVNPR(V)	
1502.8900	1502.7525	91.5194	166	178	(K)MINLSVPDTIDER(T)	
1585.9400	1585.8477	58.1710	597	610	(R)YYALPEDLVEVNPK(M)	
1758.0100	1757.8744	77.1528	310	326	(K)GDEEGIPAVVIDMSGLR(E)	

7 unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900 1689.9700

The matched peptides cover 16% (104/627 AA's) of the protein.
Coverage Map for This Hit (MS-Digest index #): 746520

FIG. 14C

MS-Tag Search Results

Sample ID (comment): Aps A-1 1040-AKPYLHDLR
 Database searched: NCBItr.51403
 Molecular weight search (1000 - 200000 Da) selects 1421445 entries.
 Full pI range: 1421416 entries.
 Species search (HUMAN/RODENT) selects 224837 entries.
 Combined molecular weight, pI and species searches select 122537 entries.
 Number of sequences passing through parent mass filter: 1727
 MS-Tag length selects 6 entries.
 Parent mass: 1287.6700 (± 0.2000 Da)
 Fragment ions used in search: 175.00, 155.28, 172.30, 301.48, 369.37, 432.69, 542.65, 633.34, 655.97, 742.67, 840.69 (± 0.70 Da)
 Ion Types Considered: a b B y n h

Search Mode Identify	Match # (unmatched ions)	Peptide Masses (are monoisotopic)	Digest Used Trypsin	Max. # Missed Cleavages 1	Cysteine Modified by acrylamide	Peptide Neutralities Hydrogen (H)	Peptide Charged Free Acid (O H)
	2						

Result Summary

Rank	# Unmatched Ions	Sequence	Mass Calculated (Da)	Mass Error (Da)	Protein MW (Da) pI	Species	NCBItr.51403 Accession #	Protein Name
1	1/11	(R)NWMNSLGYNPR(V)	1287.6268	0.1432	70288.8 / 5.29	HOMO SAPIENS	8117500	bA139H14.1 (lymphocyte cytosolic protein 1 (L-plasin))
1	1/11	(R)NWMNSLGYNPR(V)	1287.6268	0.1432	70289.7 / 5.20	HOMO SAPIENS	4501965	lymphocyte cytosolic protein 1 (L-plasin)
1	1/11	(R)NWMNSLGYNPR(V)	1287.6268	0.1432	70201.8 / 5.18	MUS MUSCULUS	6679385	63-kDa macrophage protein
1	1/11	(R)NWMNSLGYNPR(V)	1287.6268	0.1432	31331.4 / 8.60	MUS MUSCULUS	12841863	unnamed protein product
1	1/11	(R)NWMNSLGYNPR(V)	1287.6268	0.1432	70163.8 / 5.24	MUS MUSCULUS	16316929	unnamed protein product
1	1/11	(R)NWMNSLGYNPR(V)	1287.6268	0.1432	70149.7 / 5.20	MUS MUSCULUS	19840803	unnamed protein product

Detailed Results

Rank	# Unmatched Ions	Sequence	Mass Calculated (Da)	Mass Error (Da)	Protein MW (Da) pI	Species	NCBItr.51403 Accession #	MS-Digest Index #	Protein Name
1	1/11	(R)NWMNSLGYNPR(V)	1287.6268	0.1432	70288.8 / 5.29	HOMO SAPIENS	8117500	696263	bA139H14.1 (lymphocyte cytosolic protein 1 (L-plasin))
1	1/11	(R)NWMNSLGYNPR(V)	1287.6268	0.1432	70289.7 / 5.20	HOMO SAPIENS	4501965	725492	lymphocyte cytosolic protein 1 (L-plasin)
1	1/11	(R)NWMNSLGYNPR(V)	1287.6268	0.1432	70201.8 / 5.18	MUS MUSCULUS	6679385	746510	63-kDa macrophage protein
1	1/11	(R)NWMNSLGYNPR(V)	1287.6268	0.1432	31331.4 / 8.60	MUS MUSCULUS	12841863	1146922	unnamed protein product
1	1/11	(R)NWMNSLGYNPR(V)	1287.6268	0.1432	70163.8 / 5.24	MUS MUSCULUS	16316929	1174311	unnamed protein product
1	1/11	(R)NWMNSLGYNPR(V)	1287.6268	0.1432	70149.7 / 5.20	MUS MUSCULUS	19840803	171710	unnamed protein product

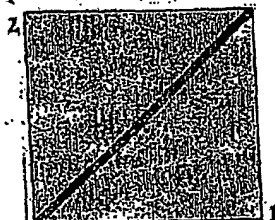
Fragment-Ion (m/z)	175.00	155.28	172.30	301.48	369.37	432.69	542.65	633.34	655.97	742.67	840.69
Ion-type	y ₁	y ₂ -NH ₂	y ₂	b ₂	y ₁ -NH ₂	b ₃	y ₁	b ₂	y ₆	y ₇	
Delta Da	0.12	0.13	0.13	0.33	0.18	0.52	0.34	0.09	0.58	0.25	

FIG. 15A

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4

Matrix: BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.00 wordsize: 3 Filter F

Sequence 1 gi 17865718 Heat shock protein HSP 90-beta (HSP 84) (HSP 90) Length 724 (1..724)
 Sequence 2 gi 72223 heat shock protein 84 - mouse Length 724 (1..724)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1178 bits (3047), Expect = 0.0
 Identities = 616/724 (85%), Positives = 616/724 (85%)

```

Query: 1  MPXXXXXXXXXXKTFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIRYESLT 60
           MP                TFAFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIRYESLT
Sbjct: 1  MP EEVHHGEEVETTFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIRYESLT 60

Query: 61  DPSKLDGKELKIDIIIPNPQERTLTLDVTGIGMTKADLINNLGTIAKSGTKAFMEALQAG 120
           DPSKLDGKELKIDIIIPNPQERTLTLDVTGIGMTKADLINNLGTIAKSGTKAFMEALQAG
Sbjct: 61  DPSKLDGKELKIDIIIPNPQERTLTLDVTGIGMTKADLINNLGTIAKSGTKAFMEALQAG 120

Query: 121  ADISMIGQFGVGFYSAYLVAEKVVVITKHNDDEQYAWESSAGGSFTVRADHGEPIGRGK 180
           ADISMIGQFGVGFYSAYLVAEKVVVITKHNDDEQYAWESSAGGSFTVRADHGEPIGRGK
Sbjct: 121  ADISMIGQFGVGFYSAYLVAEKVVVITKHNDDEQYAWESSAGGSFTVRADHGEPIGRGK 180

Query: 181  VILHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEKXXXXXXXXXXXXXXXXXXXX 240
           VILHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEK
Sbjct: 181  VILHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEKFKREKESIDEAEKEKERE 240

Query: 241  XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIDQEELNRTKPIWTRNPDDITQEE 300
           YIDQEELNRTKPIWTRNPDDITQEE
Sbjct: 241  DKEDDEKPKIEDVGSDEEDDSGDKKKKTKKIKKXIDQEELNRTKPIWTRNPDDITQEE 300

Query: 301  YGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKQNNIKLYVRRV 360
           YGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKQNNIKLYVRRV
Sbjct: 301  YGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKQNNIKLYVRRV 360

Query: 361  FIMDSCELIPEYLNFIIRGVVDSLELNISREMLQSKILKVIKNIIVKCKLELFSELA 420

```

FIG. 15B

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      FINDSCDELIPEYLNFIK  SEDLPINISREMLQQSKILKVIKKNIVKKCI  SELA
Sbjct: 361 FIMDSCELIPEYLNFIKGVDSEDLPINISREMLQQSKILKVIKKNIVKKCLLDFSELA 470

Query: 421 EDKENYKKFYEAAPSKNLKLGIHEDSTNRRRLSELLRYHTSQSGDEMTSLSEYVSRMKETQ 480
      EDKENYKKFYEAAPSKNLKLGIHEDSTNRRRLSELLRYHTSQSGDEMTSLSEYVSRMKETQ
Sbjct: 421 EDKENYKKFYEAAPSKNLKLGIHEDSTNRRRLSELLRYHTSQSGDEMTSLSEYVSRMKETQ 480

Query: 481 KSIYYITGESKEQVANSAPVERVRKRGFEVVMTEPIDEYCVQQLKEFDGKSLSVTXX 540
      KSIYYITGESKEQVANSAPVERVRKRGFEVVMTEPIDEYCVQQLKEFDGKSLSVT
Sbjct: 481 KSIYYITGESKEQVANSAPVERVRKRGFEVVMTEPIDEYCVQQLKEFDGKSLSVTKEG 540

Query: 541 XXXXXXXXXXXXXXXXXXXXNLCMLKEILDKKVEKVTISNRLVSSPCCIVTSTYGWA 600
      NLCMLKEILDKKVEKVTISNRLVSSPCCIVTSTYGWA
Sbjct: 541 LRLPEDEEEKKIMRESKAKFENLCKLMKEILDKKVEKVTISNRLVSSPCCIVTSTYGWA 600

Query: 601 NNERIMKAQALRDNSTMGYMAKKHLEINPDHFIVETLRQKAEADKNDKAVKDLVLLFE 660
      NNERIMKAQALRDNSTMGYMAKKHLEINPDHFIVETLRQKAEADKNDKAVKDLVLLFE
Sbjct: 601 NNERIMKAQALRDNSTMGYMAKKHLEINPDHFIVETLRQKAEADKNDKAVKDLVLLFE 660

Query: 661 TALLSSQFSLEDPQTHSNRIYRMIKLGLGIXXXXXXXXXXXXXXXXXXIPPLEGDEDASRM 720
      TALLSSQFSLEDPQTHSNRIYRMIKLGLGI IPPLEGDEDASRM
Sbjct: 661 TALLSSQFSLEDPQTHSNRIYRMIKLGLGIDEVTAEPSSAAVPEIPPLEGDEDASRM 720

Query: 721 EEVD 724
      EEVD
Sbjct: 721 EEVD 724

CPU time:      0.15 user secs.      0.06 sys. secs      0.21 total secs.

Lambda      K      H
      0.317      0.115      0.375

Gapped
Lambda      K      H
      0.267      0.0410      0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 4890
Number of Sequences: 0
Number of extensions: 325
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 724
length of database: 405,742,523
effective HSP length: 134
effective length of query: 590
effective length of database: 405,742,389
effective search space: 239388009510
effective search space used: 239388009510
T: 9
A: 40
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)

S1: 41 (21.6 bits)
S2: 78 (34.7 bits)

```

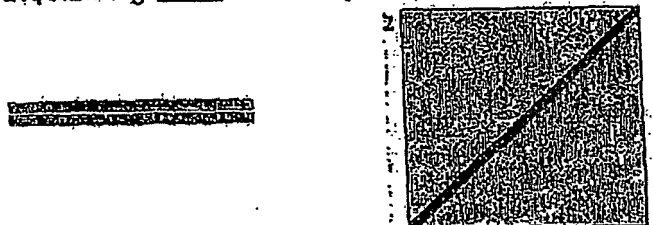
FIG. 16A

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4

Matrix: BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.00 wordsize: 3 Filter: T

Sequence 1 gi 72220 heat shock protein 86 - mouse Length 733 (1..733)

Sequence 2 gi 72223 heat shock protein 84 - mouse Length 724 (1..724)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1102 bits (2851), Expect = 0.0
 Identities = 564/733 (76%), Positives = 611/733 (82%), Gaps = 9/733 (1%)

Query: 1 MPDETQTQDQPMEESEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIR 60
 MPDE BEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIR
 Sbjct: 1 MPDEVRHG-----BEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIR 55

Query: 61 YESLTDPSKLDGSGKELHINLIPSKODRTLTIIVDTGIGMTKADLINNLGTIAKSGTKAFME 120
 YESLTDPSKLDGSGKEL I++IP+ Q+RTLT+VDTGIGMTKADLINNLGTIAKSGTKAFME
 Sbjct: 56 YESLTDPSKLDGSGKELKIDYIPNPQERTLTIVDTGIGMTKADLINNLGTIAKSGTKAFME 115

Query: 121 ALQAGADISMIGQFGVGFSAYLVAEKVTVITKHNDDEQYANESSAGGSFTVRIDGEPM 180
 ALQAGADISMIGQFGVGFSAYLVAEKV VITKHNDDEQYANESSAGGSFTVR D GEP+
 Sbjct: 116 ALQAGADISMIGQFGVGFSAYLVAEKVVVITKHNDDEQYANESSAGGSFTVRADHGEP 175

Query: 161 GRGTKVILHLKEDQTEYLEERRIKETVKKHSQFIGYPITLFVEKERXXXXXXXXXXXXX 240
 GRGTKVILHLKEDQTEYLEERR+KE+VKKHSQFIGYPITL++EKER
 Sbjct: 176 GRGTKVILHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEKEREREKESDDEABEBKG 235

Query: 241 XXX 300
 LNKTKPIINTR
 Sbjct: 236 EKEEEDKEDEKPKIEDVGSDEEDDSGDKKKKTKKIKIKYIDQE-----LNKTKPIINTR 291

Query: 301 NPDDITNEEYGEFYKSLTNDWEHLAVKHFSVEGQLEFRALLFVPRRAPFDLFENRKKQN 360
 NPDDIT EEEYGEFYKSLTNDWE+HLAVKHFSVEGQLEFRALLF+PRRAPFDLPEN+KKKN
 Sbjct: 292 NPDDITQEEYGEFYKSLTNDWEHLAVKHFSVEGQLEFRALLFVPRRAPFDLFENRKKQN 351

Query: 361 NIKLYVRRVFIMDNCEBLIPEYLNEIRGVVDSDELPLNISREMLQQSKILKVIKKNLVKK 420

FIG. 16B

```

      NIKLYVRRVFMDC+CL. :LNFIRGVVDSDDLPLNISREMLQQSKILKVI +VKK
Sbjct: 352 NIKLYVRRVFMDCDELIRSYLNFIRGVVDSDDLPLNISREMLQQSKILKVI+NIVKK 411

Query: 421 CLELFTELAEDKENYKKFYEQFSKNIKLGIBEDSQNRKQLSELLRYTTSASGDEMVS LKD 480
      CLELF+ELAEDKENYKKFYE PSKN+KLGIBEDS NR++LSELLRY+TS SGOEM SL +
Sbjct: 412 CLELPSELAEDKENYKKFYEAFSKNIKLGIBEDSTNRRRLSELLRYHTSQSODENTSLSLSE 471

Query: 481 YCTRMKENQKHIIYFITGETKQVANSAPVERLRKHGCLVYIMIEPIDEYCVQQLKEFEKG 540
      Y +RMKE QK IY+ITGS+K+QVANSAPVER+RK G EV+YM EPIDEYCVQQLKEP+CK
Sbjct: 472 YVSRMKRTQKSIYYITGESKEQVANSAPVERVRKRGFEVYMTIEPIDEYCVQQLKEFQKG 531

Query: 541 TLVSVTXXXXXXXXXXXXXXXXXXXXXXXXXNLCIMKDILEKKVEKVVVSNRLVTSPPCCI 600
      +LVSVT NLCK+MK+IL+KKVEKV +SNRLV+SPCCI
Sbjct: 532 SLVSVTKEGLELPEDEEEKKKMEESKAKFENLCKLMKEJLDKKVEKVTISNRLVSSPCCI 591

Query: 601 VTSTYGTANMERIMKAQALRDNSTMGYMAAKKHLINPDHSIIETLRQAEADKNDKSV 660
      VTSTYGTANMERIMKAQALRDNSTMGYM AKKHLINPDH I+ETLRQAEADKNDK+V
Sbjct: 592 VTSTYGTANMERIMKAQALRDNSTMGYMAKHLINPDHPIVETLRQAEADKNDKAV 651

Query: 661 KDLVILLYETALLSSGFSLEDPQTHANRIYRMIKLGLGIDEDDPTVDDTSAAVTEEMPPL 720
      KDLV+LL+ETALLSSGFSLEDPQTH+NRIYRMIKLGLGIDED+ T ++ SAAV +E+PEL
Sbjct: 652 KDLVLLPETALLSSGFSLEDPQTHSNRIYRMIKLGLGIOEDVTAREPSAAVPDEIFPL 711

Query: 721 EGDDDTSRMEEVD 733
      EGD+O SRMEEVD
Sbjct: 712 EGDDEASRMEEVD 724

CPU time: 0.17 user secs. 0.01 sys. secs 0.18 total secs.

Lambda K H
0.316 0.134 0.372

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DS: 5349
Number of Sequences: 0
Number of extensions: 384
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 733
length of database: 405,742,523
effective HSP length: 134
effective length of query: 599
effective length of database: 405,742,389
effective search space: 243039691011
effective search space used: 243039691011
T: 9
A: 40
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)

S1: 41 (21.6 bits)
S2: 78 (34.7 bits)

```